MAQAGRTGYDNREIVMKYIHYKLSQRGYEWDVGDVDAAPLG
AAPTPGIFSFQPESNPTPAVHRDMAARTSPLRPIVATTGPT
LSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTA
RGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMS
PLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSVRP
LFDFSWLSLKTLLSLALVGACITLGTYLGHK (SEQ
ID NO: 1)

FIG. 1

MAQAGRTGYDNREIVMKYIHYKLSQRGYEWDVGDVDAA**AAA**

ASPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTA

RGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMS

PLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSVRP

LFDFSWLSLKTLLSLALVGACITLGTYLGHK (SEQ ID NO: 2)

FIG. 2

```
  1 ATGGCTCAAG CTGGGAGAAC AGGGTATGAT AACCGAGAGA TCGTGATGAA
 51 GTACATCCAT TATAAGCTGT CACAGAGGGG CTACGAGTGG GATGTGGGAG
101 ATGTGGACGC CGCGGCCGCG GCCGCGAGCC CCGTGCCACC TGTGGTCCAC
151 CTGACCCTCC GCCGGGCTGG GGATGACTTC TCCCGTCGCT ACCGTCGCGA
201 CTTCGCGGAG ATGTCCAGTC AGCTGCACCT GACGCCCTTC ACCGCGAGGG
251 GACGCTTTGC TACGGTGGTG GAGGAACTCT TCAGGGATGG GGTGAACTGG
301 GGGAGGATTG TGGCCTTCTT TGAGTTCGGT GGGGTCATGT GTGTGGAGAG
351 CGTCAACAGG GAGATGTCAC CCCTGGTGGA CAACATCGCC CTGTGGATGA
401 CCGAGTACCT GAACCGGCAT CTGCACACCT GGATCCAGGA TAACGGAGGC
451 TGGGACGCAT TTGTGGAACT GTACGGCCCC AGTGTGAGGC CTCTGTTTGA
501 TTTCTCTTGG CTGTCTCTGA AGACCCTGCT CAGCCTGGCC CTGGTCGGGG
551 CCTGCATCAC TCTGGGTACC TACCTGGGCC ACAAGTGA
```

(SEQ ID NO: 3)

FIG. 3

MRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFE
PPTLHELHDLDVTAPEDPNEEAVSQIFPDSVMLAVQEGI
DLLTFPPAPGSPEPPHLSRQPEQPEQRALGPVSMPNLVP
EVIDLTGHEAGFPPSDDEDEEGEEFVLDYVEHPGHGCR
SCHYHRRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPE
PEPEPEPARPTRRPKMAPAILRRPTSPVSRECNSSTDSCD
SGPSNTPPEIHPVVPLCPIKPVAVRVGGRRQAVECIEDL
LNEPGQPLDLSCKRPRP (SEQ ID NO: 4)

FIG. 4

```
   1 ATGAGACATA TTATCTGCCA CGGAGGTGTT ATTACCGAAG AAATGGCCGC
  51 CAGTCTTTTG GACCAGCTGA TCGAAGAGGT ACTGGCTGAT AATCTTCCAC
 101 CTCCTAGCCA TTTTGAACCA CCTACCCTTC ACGAACTGCA TGATTTAGAC
 151 GTGACGGCCC CCGAAGATCC CAACGAGGAG GCGGTTTCGC AGATTTTTCC
 201 CGACTCTGTA ATGTTGGCGG TGCAGGAAGG GATTGACTTA CTCACTTTTC
 251 CGCCGGCGCC CGGTTCTCCG GAGCCGCCTC ACCTTTCCCG GCAGCCCGAG
 301 CAGCCGGAGC AGAGAGCCTT GGGTCCGGTT TCTATGCCAA ACCTTGTACC
 351 GGAGGTGATC GATCTTACCG GCCACGAGGC TGGCTTTCCA CCCAGTGACG
 401 ACGAGGATGA AGAGGGTGAG GAGTTTGTGT TAGATTATGT GGAGCACCCC
 451 GGGCACGGTT GCAGGTCTTG TCATTATCAC CGGAGGAATA CGGGGGACCC
 501 AGATATTATG TGTTCGCTTT GCTATATGAG GACCTGTGGC ATGTTTGTCT
 551 ACAGTAAGTG AAAATTATGG GCAGTGGGTG ATAGAGTGGT GGGTTTGGTG
 601 TGGTAATTTT TTTTTTAATT TTTACAGTTT TGTGGTTTAA AGAATTTTGT
 651 ATTGTGATTT TTTTAAAAGG TCCTGTGTCT GAACCTGAGC CTGAGCCCGA
 701 GCCAGAACCG GAGCCTGCAA GACCTACCCG CCGTCCTAAA ATGGCGCCTG
 751 CTATCCTGAG ACGCCCGACA TCACCTGTGT CTAGAGAATG CAATAGTAGT
 801 ACGGATAGCT GTGACTCCGG TCCTTCTAAC ACACCTCCTG AGATACACCC
 851 GGTGGTCCCG CTGTGCCCCA TTAAACCAGT TGCCGTGAGA GTTGGTGGGC
 901 GTCGCCAGGC TGTGGAATGT ATCGAGGACT TGCTTAACGA GCCTGGGCAA
 951 CCTTTGGACT TGAGCTGTAA ACGCCCCAGG CCATAA
```

(SEQ ID NO: 5)

FIG. 5

```
  1 GAATTCGCCG CCACCATGGA GGCTTGGGAG TGTTTGGAAG ATTTTTCTGC
 51 TGTGCGTAAC TTGCTGGAAC AGAGCTCTAA CAGTACCTCT TGGTTTTGGA
101 GGTTTCTGTG GGGCTCATCC CAGGCAAAGT TAGTCTGCAG AATTAAGGAG
151 GATTACAAGT GGGAATTTGA AGAGCTTTTG AAATCCTGTG GTGAGCTGTT
201 TGATTCTTTG AATCTGGGTC ACCAGGCGCT TTTCCAAGAG AAGGTCATCA
251 AGACTTTGGA TTTTTCCACA CCGGGGCGCG CTGCGGCTGC TGTTGCTTTT
301 TTGAGTTTTA TAAAGGATAA ATGGAGCGAA GAAACCCATC TGAGCGGGGG
351 GTACCTGCTG GATTTTCTGG CCATGCATCT GTGGAGAGCG GTTGTGAGAC
401 ACAAGAATCG CCTGCTACTG TTGTCTTCCG TCCGCCCGGC GATAATACCG
451 ACGGAGGAGC AGCAGCAGCA GCAGGAGGAA GCCAGGCGGC GGCGGCAGGA
501 GCAGAGCCCA TGGAACCCGA GAGCCGGCCT GGACCCTCGG GAATGAATGT
551 TGGTCGAC          (SEQ ID NO: 15)
```

FIG. 6

```
   SalI
 1 GTCGACGCCG CCACCATGCC GCCCAAAACC CCCCGAAAAA CGGCCGCCAC
                     M  P   P  K  T   P  R  K  T   A  A  T

51 CGCCGCCGCT GCCGCCGCGG AACCCCCGGC ACCGCCGCCG CCGCCCCCTC
    A  A  A   A  A  A  E   P  P  A   P  P  P   P  P  P  P

101 CTGAGGAGGA CCCAGAGCAG GACAGCGGCC CGGAGGACCT GCCTCTCGTC
     E  E  D   P  E  Q   D  S  G  P   E  D  L   P  L  V

151 AGGCTTGAGT TTGAAGAAAC AGAAGAACCT GATTTTACTG CATTATGTCA
    R  L  E  F   E  E  T   E  E  P   D  F  T  A   L  C  Q

201 GAAATTAAAG ATACCAGATC ATGTCAGAGA GAGAGCTTGG TTAACTTGGG
    K  L  K   I  P  D  H   V  R  E   R  A  W   L  T  W  E

251 AGAAAGTTTC ATCTGTGGAT GGAGTATTGG GAGGTTATAT TCAAAAGAAA
     K  V  S   S  V  D   G  V  L  G   G  Y  I   Q  K  K

301 AAGGAACTGT GGGGAATCTG TATCTTTATT GCACGAGTTG ACCTAGATGA
    K  E  L  W   G  I  C   I  F  I   A  R  V  D   L  D  E

351 GATGTCGTTC ACTTTACTGA GCTACAGAAA AACATACGAA ATCAGTGTCC
     M  S  F   T  L  L  S   Y  R  K   T  Y  E   I  S  V  H

401 ATAAATTCTT TAACTTACTA AAAGAAATTG ATACCAGTAC CAAAGTTGAT
     K  F  F   N  L  L   K  E  I  D   T  S  T   K  V  D

451 AATGCTATGT CAAGACTGTT GAAGAAGTAT GATGTATTGT TTGCACTCTT
    N  A  M  S   R  L  L   K  K  Y   D  V  L  F   A  L  F

501 CAGCAAATTG GAAAGGACAT GTGAACTTAT ATATTTGACA CAACCCAGCA
     S  K  L   E  R  T  C   E  L  I   Y  L  T   Q  P  S  S

551 GTTCGATATC TACTGAAATA AATTCTGCAT TGGTGCTAAA AGTTTCTTGG
     S  I  S   T  E  I   N  S  A  L   V  L  K   V  S  W

601 ATCACATTTT TATTAGCTAA AGGGGAAGTA TTACAAATGG AAGATGATCT
    I  T  F  L   L  A  K   G  E  V   L  Q  M  E   D  D  L

651 GGTGATTTCA TTTCAGTTAA TGCTATGTGT CCTTGACTAT TTTATTAAAC
    V  I  S  F  Q  L  M   L  C  V   L  D  Y   F  I  K  L
```

FIG. 7A

```
701 TCTCACCTCC CATGTTGCTC AAAGAACCAT ATAAAACAGC TGTTATACCC
      S  P  P   M  L  L   K  E  P  Y   K  T  A   V  I  P

751 ATTAATGGTT CACCTCGAAC ACCCAGGCGA GGTCAGAACA GGAGTGCACG
    I  N  G  S   P  R  T   P  R  R   G  Q  N  R   S  A  R

801 GATAGCAAAA CAACTAGAAA ATGATACAAG AATTATTGAA GTTCTCTGTA
      I  A  K   Q  L  E  N   D  T  R   I  I  E   V  L  C  K

851 AAGAACATGA ATGTAATATA GATGAGGTGA AAAATGTTTA TTTCAAAAAT
      E  H  E   C  N  I   D  E  V  K   N  V  Y   F  K  N

                    EcoRI
901 TTTATACCTT TTATGAATTC TCTTGGACTT GTAACATCTA ATGGACTTCC
    F  I  P  F   M  N  S   L  G  L   V  T  S  N   G  L  P

951 AGAGGTTGAA AATCTTTCTA AACGATACGA AGAAATTTAT CTTAAAAATA
      E  V  E   N  L  S  K   R  Y  E   E  I  Y   L  K  N  K

1001 AAGATCTAGA TCGAAGATTA TTTTTGGATC ATGATAAAAC TCTTCAGACT
       D  L  D   R  R  L   F  L  D  H   D  K  T   L  Q  T

1051 GATTCTATAG ACAGTTTTGA AACACAGAGA ACACCACGAA AAAGTAACCT
     D  S  I  D   S  F  E   T  Q  R   T  P  R  K   S  N  L

1101 TGATGAAGAG GTGAATATAA TTCCTCCACA CACTCCAGTT AGGACTGTTA
       D  E  E   V  N  I  I   P  P  H   T  P  V   R  T  V  M

1151 TGAACACTAT CCAACAATTA ATGATGATTT TAAATTCTGC AAGTGATCAA
       N  T  I   Q  Q  L   M  M  I  L   N  S  A   S  D  Q

1201 CCTTCAGAAA ATCTGATTTC CTATTTTAAC AACTGCACAG TGAATCCAAA
     P  S  E  N   L  I  S   Y  F  N   N  C  T  V   N  P  K

1251 AGAAAGTATA CTGAAAAGAG TGAAGGATAT AGGATACATC TTTAAAGAGA
       E  S  I   L  K  R  V   K  D  I   G  Y  I   F  K  E  K

1301 AATTTGCTAA AGCTGTGGGA CAGGGTTGTG TCGAAATTGG ATCACAGCGA
       F  A  K   A  V  G   Q  G  C  V   E  I  G   S  Q  R

1351 TACAAACTTG GAGTTCGCTT GTATTACCGA GTAATGGAAT CCATGCTTAA
     Y  K  L  G   V  R  L   Y  Y  R  V   M  E  S   M  L  K
```

FIG. 7B

```
1401 ATCAGAAGAA GAACGATTAT CCATTCAAAA TTTTAGCAAA CTTCTGAATG
       S  E  E   E  R  L  S   I  Q  N   F  S  K   L  L  N  D

1451 ACAACATTTT TCATATGTCT TTATTGGCGT GCGCTCTTGA GGTTGTAATG
       N  I  F   H  M  S   L  L  A  C   A  L  E   V  V  M

1501 GCCACATATA GCAGAAGTAC ATCTCAGAAT CTTGATTCTG GAACAGATTT
       A  T  Y   S  R  S   T  S  Q  N   L  D  S   G  T  D  L

1551 GTCTTTCCCA TGGATTCTGA ATGTGCTTAA TTTAAAAGCC TTTGATTTTT
       S  F  P   W  I  L   N  V  L  N   L  K  A   F  D  F  Y

1601 ACAAAGTGAT CGAAAGTTTT ATCAAAGCAG AAGGCAACTT GACAAGAGAA
       K  V  I   E  S  F   I  K  A  E   G  N  L   T  R  E

1651 ATGATAAAAC ATTTAGAACG ATGTGAACAT CGAATCATGG AATCCCTTGC
       M  I  K   H  L  E   R  C  E  H   R  I  M   E  S  L  A

1701 ATGGCTCTCA GATTCACCTT TATTTGATCT TATTAAACAA TCAAAGGACC
       W  L  S   D  S  P   L  F  D  L   I  K  Q   S  K  D  R

1751 GAGAAGGACC AACTGATCAC CTTGAATCTG CTTGTCCTCT TAATCTTCCT
       E  G  P   T  D  H   L  E  S  A   C  P  L   N  L  P

1801 CTCCAGAATA ATCACACTGC AGCAGATATG TATCTTTCTC CTGTAAGATC
       L  Q  N   N  H  T   A  A  D  M   Y  L  S   P  V  R  S

1851 TCCAAAGAAA AAAGGTTCAA CTACGCGTGT AAATTCTACT GCAAATGCAG
       P  K  K   K  G  S   T  T  R  V   N  S  T   A  N  A  E

1901 AGACACAAGC AACCTCAGCC TTCCAGACCC AGAAGCCATT GAAATCTACC
       T  Q  A   T  S  A   F  Q  T  Q   K  P  L   K  S  T

1951 TCTCTTTCAC TGTTTTATAA AAAAGTGTAT CGGCTAGCCT ATCTCCGGCT
       S  L  S   L  F  Y   K  K  V  Y   R  L  A   Y  L  R  L

2001 AAATACACTT TGTGAACGCC TTCTGTCTGA GCACCCAGAA TTAGAACATA
       N  T  L   C  E  R   L  L  S  E   H  P  E   L  E  H  I

2051 TCATCTGGAC CCTTTTCCAG CACACCCTGC AGAATGAGTA TGAACTCATG
       I  W  T   L  F  Q   H  T  L  Q   N  E  Y   E  L  M
```

FIG. 7C

```
2101 AGAGACAGGC ATTTGGACCA AATTATGATG TGTTCCATGT ATGGCATATG
       R  D  R  H     L  D  Q     I  M  M     C  S  M  Y     G  I  C

2151 CAAAGTGAAG AATATAGACC TTAAATTCAA AATCATTGTA ACAGCATACA
       K  V  K     N  I  D  L     K  F  K     I  I  V     T  A  Y  K

2201 AGGATCTTCC TCATGCTGTT CAGGAGACAT TCAAACGTGT TTTGATCAAA
       D  L  P     H  A  V     Q  E  T  F     K  R  V     L  I  K

2251 GAAGAGGAGT ATGATTCTAT TATAGTATTC TATAACTCGG TCTTCATGCA
       E  E  E  Y     D  S  I     I  V  F     Y  N  S  V     F  M  Q

2301 GAGACTGAAA ACAAATATTT TGCAGTATGC TTCCACCAGG CCCCCTACCT
       R  L  K     T  N  I  L     Q  Y  A     S  T  R     P  P  T  L

2351 TGTCACCAAT ACCTCACATT CCTCGAAGCC CTTACAAGTT TCCTAGTTCA
       S  P  I     P  H  I     P  R  S  P     Y  K  F     P  S  S

2401 CCCTTACGGA TTCCTGGAGG GAACATCTAT ATTTCACCCC TGAAGAGTCC
       P  L  R  I     P  G  G     N  I  Y     I  S  P  L     K  S  P

2451 ATATAAAATT TCAGAAGGTC TGCCAACACC AACAAAAATG ACTCCAAGAT
       Y  K  I     S  E  G  L     P  T  P     T  K  M     T  P  R  S

2501 CAAGAATCTT AGTATCAATT GGTGAATCAT TCGGGACTTC TGAGAAGTTC
       R  I  L     V  S  I     G  E  S  F     G  T  S     E  K  F

2551 CAGAAAATAA ATCAGATGGT ATGTAACAGC GACCGTGTGC TCAAAAGAAG
       Q  K  I  N     Q  M  V     C  N  S     D  R  V  L     K  R  S

2601 TGCTGAAGGA AGCAACCCTC CTAAACCACT GAAAAAACTA CGCTTTGATA
       A  E  G     S  N  P  P     K  P  L     K  K  L     R  F  D  I

2651 TTGAAGGATC AGATGAAGCA GATGGAAGTA AACATCTCCC AGGAGAGTCC
       E  G  S     D  E  A     D  G  S  K     H  L  P     G  E  S

2701 AAATTTCAGC AGAAACTGGC AGAAATGACT TCTACTCGAA CACGAATGCA
       K  F  Q  Q     K  L  A     E  M  T     S  T  R  T     R  M  Q

2751 AAAGCAGAAA ATGAATGATA GCATGGATAC CTCAAACAAG GAAGAGAAAT
       K  Q  K     M  N  D  S     M  D  T     S  N  K     E  E  K  *

                          NotI
2801 GAGGATCTCA GGACCGGCGG CCGC
```

FIG. 7D

```
    EcoRI
  1 GAATTCGCCG CCACCATGAC CATGGACTCT GGAGCAGACA ACCAGCAGAG
                      M  T   M  D  S   G  A  D  N   Q  Q  S

 51 TGGAGATGCA GCTGTAACAG AAGCTGAAAA CCAACAAATG ACAGTTCAAG
      G  D  A   A  V  T  E   A  E  N   Q  Q  M   T  V  Q  A

101 CCCAGCCACA GATTGCCACA TTAGCCCAGG TATCTATGCC AGCAGCTCAT
      Q  P  Q   I  A  T   L  A  Q  V   S  M  P   A  A  H

151 GCAACATCAT CTGCTCCCAC CGTAACTCTA GTACAGCTGC CCAATGGGCA
    A  T  S  S   A  P  T   V  T  L   V  Q  L  P   N  G  Q

201 GACAGTTCAA GTCCATGGAG TCATTCAGGC GGCCCAGCCA TCAGTTATTC
      T  V  Q   V  H  G  V   I  Q  A   A  Q  P   S  V  I  Q

251 AGTCTCCACA AGTCCAAACA GTTCAGATTT CAACTATTGC AGAAAGTGAA
      S  P  Q   V  Q  T   V  Q  I  S   T  I  A   E  S  E

301 GATTCACAGG AGTCAGTGGA TAGTGTAACT GATTCCCAAA AGCGAAGGGA
    D  S  Q  E   S  V  D   S  V  T   D  S  Q  K   R  R  E

351 AATTCTTTCA AGGAGGCCTT CCTTCAGGAA AATTTTGAAT GACTTATCTT
    I  L  S   R  R  P  S   F  R  K   I  L  N   D  L  S  S

401 CTGATGCACC AGGAGTGCCA AGGATTGAAG AAGAGAAGTC TGAAGAGGAG
      D  A  P   G  V  P   R  I  E  E   E  K  S   E  E  E

451 GCTTCAGCAC CTGCCATCAC CGCTGTAGCG GTGCCAACGC CAATTTACCG
    A  S  A  P   A  I  T   A  V  A   V  P  T  P   I  Y  R

501 GACTAGCAGT GGACAGTATA TTACCATTAC CCAGAGAGGA GCAATACAGC
      T  S  S   G  Q  Y  I   T  I  T   Q  R  G   A  I  Q  L

551 TGGCTAGCAA TGGTACCGAT GGGGTACAGG GCCTGCAAAC ATTAACCATG
      A  S  N   G  T  D   G  V  Q  G   L  Q  T   L  T  M

601 GCCAATGCAG CAGCCACTCA GCCGGGTACT ACCATTCTAC AGTATGCACA
    A  N  A  A   A  T  Q   P  G  T   T  I  L  Q   Y  A  Q

651 GACCACTGAT GGACAGCAGA TCTTAGTGCC CAGCAACCAA GTTGTTGTTC
      T  T  D   G  Q  Q  I   L  V  P   S  N  Q   V  V  V  Q
```

FIG. 8A

```
701 AAGCTGCCTC TGGAGACGTA CAAACATACC AGATTCGCAC AGCACCCACT
      A  A  S   G  D  V   Q  T  Y  Q   I  R  T   A  P  T

751 AGCACTATTG CCCCTGGAGT TGTTATGGCA TCCTCCCCAG CACTTCCTAC
    S  T  I  A   P  G  V   V  M  A   S  S  P  A   L  P  T

801 ACAGCCTGCT GAAGAAGCAG CACGAAAGAG AGAGGTCCGT CTAATGAAGA
     Q  P  A   E  E  A  A   R  K  R   E  V  R   L  M  K  N

851 ACAGGGAAGC AGCTCGTGAG TGTCGTAGAA AGAAGAAAGA ATATGTGAAA
      R  E  A   A  R  E   C  R  R  K   K  K  E   Y  V  K

901 TGTTTAGAAA ACAGAGTGGC AGTGCTTGAA AATCAAAACA AGACATTGAT
    C  L  E  N   R  V  A   V  L  E  N  Q  N  K   T  L  I

951 TGAGGAGCTA AAAGCACTTA AGGACCTTTA CTGCCACAAA TCAGATTAAT
     E  E  L   K  A  L  K   D  L  Y   C  H  K   S  D  *

        SalI
1001 TTGGGTCGAC
```

FIG. 8B

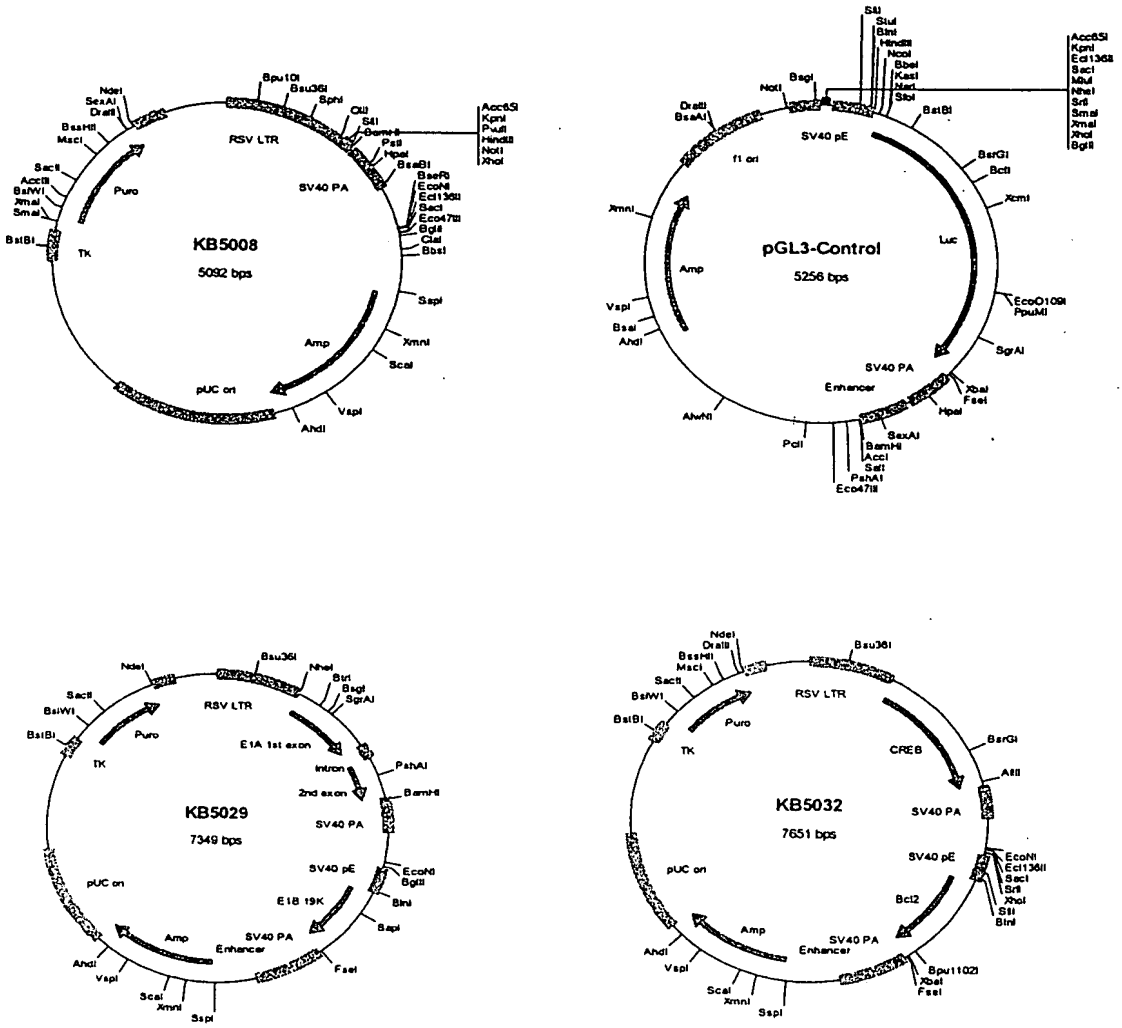

Figure 9. Maps of KB5008, pGL3-Control, KB5029, and KB5032.

KB5008 carries a RSVLTR promoter and was used to clone E1a and CREB. pGL3-Control carries a SV40 promoter and was used to clone E1b-19K and Bcl2. KB5029 carries the double expression cassettes for E1a and E1b-19K. KB5032 carries the double expression cassettes for CREB and Bcl2.

1 aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
HindIII M R H I I C H G G V I

51 cgaagaaatg gccgccagtc ttttggacca gctgatcgaa gaggtactgg
T E E M A A S L L D Q L I E E V L

101 ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
A D N L P P P S H F E P P T L H E

151 ctgtatgatt tagacgtgac ggcccccgaa gatcccaacg aggaggcggt
L Y D L D V T A P E D P N E E A

201 ttcgcagatt tttcccgact ctgtaatgtt ggcggtgcag gaagggattg
V S Q I F P D S V M L A V Q E G I

251 acttactcac ttttccgccg gcgcccggtt ctccggagcc gcctcacctt
D L L T F P P A P G S P E P P H L

301 tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat
S R Q P E Q P E Q R A L G P V S

351 gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggctggct
M P N L V P E V I D L T C H E A G

401 ttccacccag tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
F P P S D D E D E E G E E F V L D

451 tatgtggagc accccgggca cggttgcagg tcttgtcatt atcaccggag
Y V E H P G H G C R S C H Y H R

501 gaatacgggg gacccagata ttatgtgttc gctttgctat atgaggacct
R N T G D P D I M C S L C Y M R T

551 gtggcatgtt tgtctacagt cctgtgtctg aacctgagcc tgagcccgag
C G M F V Y S P V S E P E P E P E

601 ccagaaccgg agcctgcaag acctacccgc cgtcctaaaa tggcgcctgc
P E P E P A R P T R R P K M A P

651 tatcctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
A I L R R P T S P V S R E C N S S

701 cggatagctg tgactccggt ccttctaaca cacctcctga gatacacccg
T D S C D S G P S N T P P E I H P

751 gtggtcccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggcg
V V P L C P I K P V A V R V G G

801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
R R Q A V E C I E D L L N E P G Q

851 ctttggactt gagctgtaaa cgccccaggc cataactcga g
P L D L S C K R P R P - *XhoI*

Figure 10. Nucleotide coding sequence of E1a cDNA (SEQ ID NO: 40). Cloning sites HindIII and XhoI, and two amino acid residue positions Y47 and C124 are underscored.

1 aagcttgccg ccaccatgag acatattatc tgccacggag gtgttattac
HindIII M R H I I C H G G V I

51 cgaagaaatg gccgccagtc ttttggacca gctgatcgaa gaggtactgg
T E E M A A S L L D Q L I E E V L

101 ctgataatct tccacctcct agccattttg aaccacctac ccttcacgaa
A D N L P P P S H F E P P T L H E

151 ctgcatgatt tagacgtgac ggccccccgaa gatcccaacg aggaggcggt
L H D L D V T A P E D P N E E A

201 ttcgcagatt tttcccgact ctgtaatgtt ggcggtgcag gaagggattg
V S Q I F P D S V M L A V Q E G I

251 acttactcac ttttccgccg gcgcccggtt ctccggagcc gcctcacctt
D L L T F P P A P G S P E P P H L

301 tcccggcagc ccgagcagcc ggagcagaga gccttgggtc cggtttctat
S R Q P E Q P E Q R A L G P V S

351 gccaaacctt gtaccggagg tgatcgatct tacctgccac gaggctggct
M P N L V P E V I D L T C H E A G

401 ttccacccag tgacgacgag gatgaagagg gtgaggagtt tgtgttagat
F P P S D D E D E E G E E F V L D

451 tatgtggagc accccgggca cggttgcagg tcttgtcatt atcaccggag
Y V E H P G H G C R S C H Y H R

501 gaatacgggg gacccagata ttatgtgttc gctttgctat atgaggacct
R N T G D P D I M C S L C Y M R T

551 gtggcatgtt tgtctacagt cctgtgtctg aacctgagcc tgagcccgag
C G M F V Y S P V S E P E P E P E

601 ccagaaccgg agcctgcaag acctacccgc cgtcctaaaa tggcgcctgc
P E P E P A R P T R R P K M A P

651 tatcctgaga cgcccgacat cacctgtgtc tagagaatgc aatagtagta
A I L R R P T S P V S R E C N S S

701 cggatagctg tgactccggt ccttctaaca cacctcctga gatacacccg
T D S C D S G P S N T P P E I H P

751 gtggtcccgc tgtgccccat taaaccagtt gccgtgagag ttggtgggcg
V V P L C P I K P V A V R V G G

801 tcgccaggct gtggaatgta tcgaggactt gcttaacgag cctgggcaac
R R Q A V E C I E D L L N E P G Q

851 ctttggactt gagctgtaaa cgccccaggc cataactcga g
P L D L S C K R P R P - *XhoI*

Figure 11. Nucleotide coding sequence of E1a_Y47H (SEQ ID NO: 41). Cloning sites HindIII and XhoI are underscored.

1 aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
HindIII M T M E S G A D N Q Q

51 tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
S G D A A V T E A E N Q Q M T A Q

101 cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
A Q P Q I A T L A Q V S M P A A H

151 gcgacatcat ctgctcccac tgtaacctta gtgcagctgc ccaatgggca
A T S S A P T V T L V Q L P N G

201 gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
Q T V Q V H G V I Q A A Q P S V I

251 agtctccaca agtccaaaca gttcagtctt cctgtaagga cttaaaaaga
Q S P Q V Q T V Q S S C K D L K R

301 cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
L F S G T Q I S T I A E S E D S

351 ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
Q E S V D S V T D S Q K R R E I L

401 caaggaggcc ttcctacagg aaaattttga atgacttatc ttctgatgca
S R R P S Y R K I L N D L S S D A

451 ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
P G V P R I E E E K S E E E T S

501 ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
A P A I T T V T V P T P I Y Q T S

551 gtgggcagta tattgccatt acccagggag gagctataca gctggctaac
S G Q Y I A I T Q G G A I Q L A N

601 aatggtaccg atggggtaca gggccttcag acattaacca tgaccaatgc
N G T D G V Q G L Q T L T M T N

651 agctgccact cagccgggta ccactattct acagtatgca cagaccactg
A A A T Q P G T T I L Q Y A Q T T

701 atggacagca gattctagtg cccagcaacc aagttgttgt tcaagctgcc
D G Q Q I L V P S N Q V V V Q A A

751 tctggcgatg tacaaacata ccaaattcgt acagcaccca ctagcaccat
S G D V Q T Y Q I R T A P T S T

801 cgcccctgga gttgttatgg catcctcccc agcacttcct acgcagcctg
I A P G V V M A S S P A L P T Q P

851 ctgaagaagc agcccggaag agagaggttc gtctaatgaa gaacagggaa
A E E A A R K R E V R L M K N R E

901 gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
A A R E C R R K K K E Y V K C L

951 gaacagagtg gcagtgcttg aaaaccaaaa caagacattg attgaggagc
E N R V A V L E N Q N K T L I E E

1001 taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
L K A L K D L Y C H K S D - *BamHI*

Figure 12. Nucleotide coding sequence of hamster CREB-B cDNA (SEQ ID NO: 42). Cloning sites HindIII and BamHI are underscored.

```
1 aagcttgccg ccaccatgac catggaatct ggagcagaca accagcagag
  HindIII       M  T  M  E  S  G  A  D  N  Q  Q

51 tggagatgct gctgtaacag aagctgaaaa tcaacaaatg acagctcaag
   S  G  D  A  A  V  T  E  A  E  N  Q  Q  M  T  A  Q

101 cccaaccaca gattgccaca ttagcccagg tatccatgcc agcagctcat
    A  Q  P  Q  I  A  T  L  A  Q  V  S  M  P  A  A  H

151 gcgacatcat ctgctcccac tgtaacctta gtgcagctgc ccaatgggca
    A  T  S  S  A  P  T  V  T  L  V  Q  L  P  N  G

201 gacagtccaa gtccatggag ttattcaggc ggcccagcca tcagttattc
    Q  T  V  Q  V  H  G  V  I  Q  A  A  Q  P  S  V  I

251 agtctccaca agtccaaaca gttcagtctt cctgtaagga cttaaaaaga
    Q  S  P  Q  V  Q  T  V  Q  S  S  C  K  D  L  K  R

301 cttttctccg gaactcagat ttcaactatt gcagaaagtg aggattcaca
    L  F  S  G  T  Q  I  S  T  I  A  E  S  E  D  S

351 ggaatctgtg gatagtgtaa ctgattccca aaagcgaagg gaaattcttt
    Q  E  S  V  D  S  V  T  D  S  Q  K  R  R  E  I  L

401 caaggaggcc ttcctccagg aaaattttga atgacttatc ttctgatgca
    S  R  R  P  S  F  R  K  I  L  N  D  L  S  S  D  A

451 ccaggggtgc caaggattga agaagaaaag tcggaagagg agacttcagc
    P  G  V  P  R  I  E  E  E  K  S  E  E  E  T  S

501 ccctgccatc accactgtga cagtgccaac tccgatttac cagacaagca
    A  P  A  I  T  T  V  T  V  P  T  P  I  Y  Q  T  S

551 gtgggcagta tattgccatt acccagggag gagctataca gctggctaac
    S  G  Q  Y  I  A  I  T  Q  G  G  A  I  Q  L  A  N

601 aatggtaccg atggggtaca gggccttcag acattaacca tgaccaatgc
    N  G  T  D  G  V  Q  G  L  Q  T  L  T  M  T  N

651 agctgccact cagccgggta ccactattct acagtatgca cagaccactg
    A  A  A  T  Q  P  G  T  T  I  L  Q  Y  A  Q  T  T

701 atggacagca gattctagtg cccagcaacc aagttgttgt tcaagctgcc
    D  G  Q  Q  I  L  V  P  S  N  Q  V  V  V  Q  A  A

751 tctggcgatg tacaaacata ccaaattcgt acagcaccca ctagcaccat
    S  G  D  V  Q  T  Y  Q  I  R  T  A  P  T  S  T

801 cgccccctgga gttgttatgg catcctcccc agcacttcct acgcagcctg
    I  A  P  G  V  V  M  A  S  S  P  A  L  P  T  Q  P

851 ctgaagaagc agcccggaag agagaggttc gtctaatgaa gaacagggaa
    A  E  E  A  A  R  K  R  E  V  R  L  M  K  N  R  E

901 gcagcaagag aatgtcgtag aaagaagaaa gaatatgtga aatgtttaga
    A  A  R  E  C  R  R  K  K  K  E  Y  V  K  C  L

951 gaacagagtg gcagtgcttg aaaaccaaaa caagacattg attgaggagc
    E  N  R  V  A  V  L  E  N  Q  N  K  T  L  I  E  E

1001 taaaagcact taaggacctt tactgccaca aatcagatta aggatcc
     L  K  A  L  K  D  L  Y  C  H  K  S  D  -  BamHI
```

Figure 13. Nucleotide coding sequence of hamster CREB-B Y134F cDNA (SEQ ID NO: 43). Cloning sites HindIII and BamHI are underscored.

1 aagcttactg ttggtaaagc cgccaccatg gaggcttggg agtgtttgga
HindIII M E A W E C L

51 agatttttct gctgtgcgta acttgctgga acagagctct aacagtacct
E D F S A V R N L L E Q S S N S T

101 cttggttttg gaggtttctg tggggctcat cccaggcaaa gttagtctgc
S W F W R F L W G S S Q A K L V C

151 agaattaagg aggattacaa gtgggaattt gaagagcttt tgaaatcctg
R I K E D Y K W E F E E L L K S

201 tggtgagctg tttgattctt tgaatctggg tcaccaggcg cttttccaag
C G E L F D S L N L G H Q A L F Q

251 agaaggtcat caagactttg gatttttcca caccggggcg cgctgcggct
E K V I K T L D F S T P G R A A A

301 gctgttgctt ttttgagttt tataaaggat aaatggagcg aagaaaccca
A V A F L S F I K D K W S E E T

351 tctgagcggg gggtacctgc tggattttct ggccatgcat ctgtggagag
H L S G G Y L L D F L A M H L W R

401 cggttgtgag acacaagaat cgcctgctac tgttgtcttc cgtccgcccg
A V V R H K N R L L L L S S V R P

451 gcgataatac cgacggagga gcagcagcag cagcaggagg aagccaggcg
A I I P T E E Q Q Q Q Q E E A R

501 gcggcggcag gagcagagcc catggaaccc gagagccggc ctggaccctc
R R R Q E Q S P W N P R A G L D P

551 gggaatgatc taga
R E - *XbaI*

Figure 14. Nucleotide coding sequence of E1b-19K (SEQ ID NO: 44). **Cloning sites HindIII and XbaI are underscored.**

NcoI

1 ccatggctca agctgggaga acagggtatg ataaccgaga gatcgtgatg
M A Q A G R T G Y D N R E I V M

51 aagtacatcc attataagct gtcacagagg ggctacgagt gggatgtggg
K Y I H Y K L S Q R G Y E W D V

101 agatgtggac gccgcggccg cggccgcgag ccccgtgcca cctgtggtcc
G D V D A A A A A A S P V P P V V

151 acctgaccct ccgccgggct ggggatgact tctcccgtcg ctaccgtcgc
H L T L R R A G D D F S R R Y R R

201 gacttcgcgg agatgtccag tcagctgcac ctgacgccct tcaccgcgag
D F A E M S S Q L H L T P F T A

251 gggacgcttt gctacggtgg tggaggaact cttcagggat ggggtgaact
R G R F A T V V E E L F R D G V N

301 ggggggaggat tgtggccttc tttgagttcg gtggggtcat gtgtgtggag
W G R I V A F F E F G G V M C V E

351 agcgtcaaca gggagatgtc acccctggtg gacaacatcg ccctgtggat
S V N R E M S P L V D N I A L W

401 gaccgagtac ctgaaccggc atctgcacac ctggatccag gataacggag
M T E Y L N R H L H T W I Q D N G

451 gctgggacgc atttgtggaa ctgtacggcc ccagtgtgag gcctctgttt
G W D A F V E L Y G P S V R P L F

501 gatttctctt ggctgtctct gaagaccctg ctcagcctgg ccctggtcgg
D F S W L S L K T L L S L A L V

551 ggcctgcatc actctgggta cctacctggg ccacaagtga tctaga
G A C I T L G T Y L G H K - *XbaI*

Figure 15. Nucleotide coding sequence of hamster Bcl2 deletion mutant (SEQ ID NO: 45). Cloning sites NcoI and XbaI are underscored.

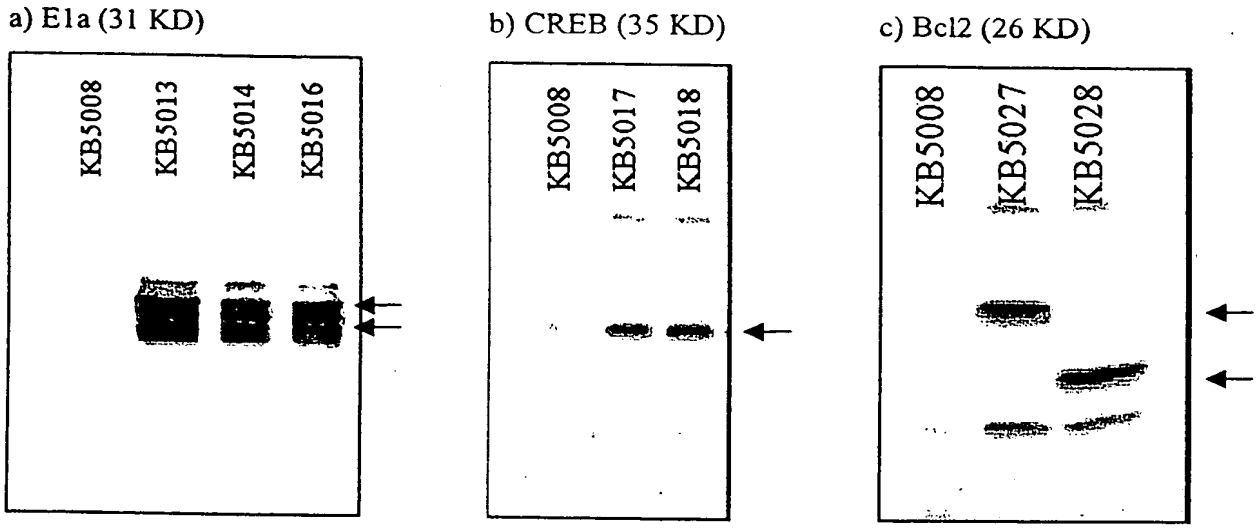

Figure 16. Western blots of E1a, CREB and Bcl2.

In a), b), and c), $1x10^5$ CHO-K1 cells were transfected with 0.4 μg of indicated plasmid DNA. Cell lysates were collected after 48 hours and probed with appropriate antibodies. KB5008 transfected cells were used as negative controles.

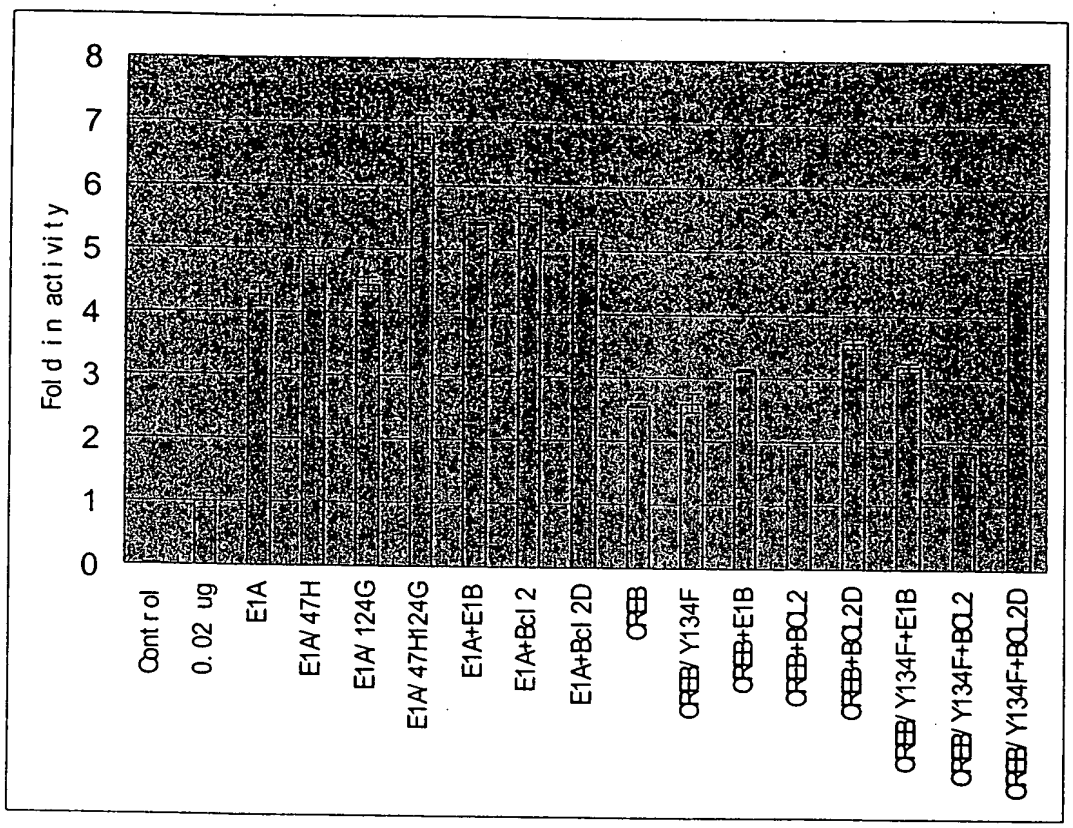

Figure 17. E1a and CREB enhanced CMV promoter in CHO-K1 cells.

$1x10^5$ cells were transfected with 0.02 μg of SEAP reporter construct KB5019 and 0.2 μg of E1a or CREB expressing constructs. Total DNA was added up to 0.4 μg/well by control plasmid KB5008, E1b-19K or Bcl2 expressing plasmids. SEAP activities from culture media were assay 48 hours after transfection. The control was mock transfected CHO-K1 cells.

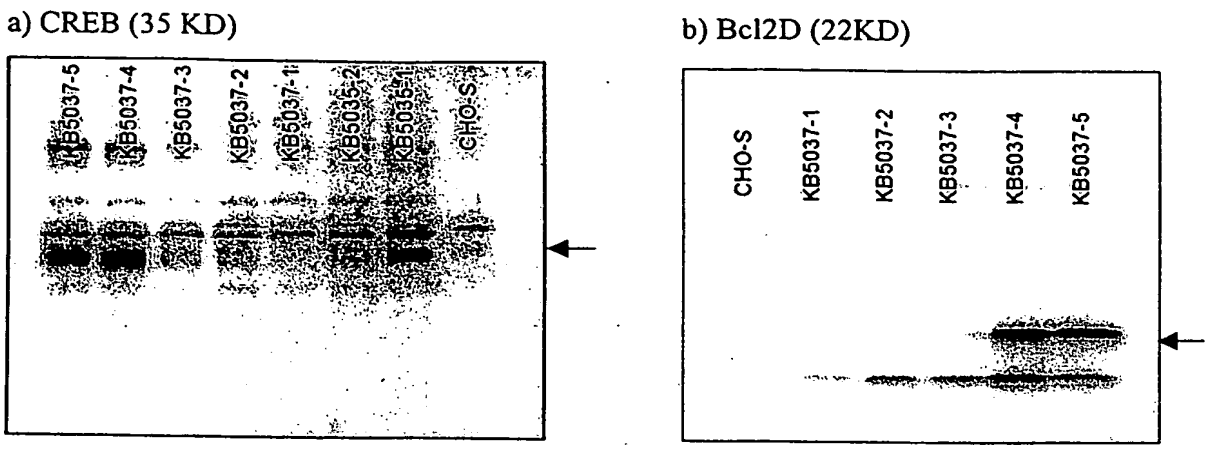

Figure 18. Western blots showing overexpression of hamster CREB-B Y134F and hamster ΔBcl-2 in stable transfectant CHO-S cell lines.